HAPLOTYPE NUMBER[a]										PS[b]	PS
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	G	G	G	2	3409
A	A	A	A	A	A	A	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
A	A	A	A	A	A	A	G	G	G	5	4054
G	G	G	G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	A	G	G	8	12356
T	T	T	T	T	T	T	T	C	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	C	C	C	C	C	C	C	C	11	12653
A	G	G	G	G	G	G	G	G	G	12	14824
A	A	A	A	A	G	G	G	A	A	13	14990
C	C	C	C	T	C	C	C	C	C	14	15089
C	C	C	T	C	C	C	C	C	C	15	15093
C	C	T	C	C	C	T	T	T	C	16	15529
G	G	G	G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]										PS[b]	PS
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	T	T	T	2	3409
A	A	A	A	G	G	G	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
G	G	G	G	A	A	A	A	A	A	5	4054
G	G	G	G	G	G	G	A	G	G	6	4082
C	C	C	T	C	C	T	C	C	C	7	11998
G	G	G	G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	T	T	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	T	C	C	C	C	T	C	C	11	12653
G	G	G	G	G	G	G	G	G	G	12	14824
A	G	A	G	A	A	A	A	A	G	13	14990
C	C	C	C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	C	C	C	15	15093
T	T	T	T	C	T	C	T	T	T	16	15529
G	G	G	G	G	G	G	G	A	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]							PS[b] NUMBER	PS POSITION[c]
21	22	23	24	25	26	27		
G	G	G	G	G	G	T	1	3102
T	T	T	T	T	T	G	2	3409
A	A	A	A	A	G	G	3	3438
C	C	C	C	G	C	C	4	3603
A	A	A	G	A	A	A	5	4054
G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	9	12397
C	C	T	C	C	C	C	10	12489
T	T	T	T	T	C	C	11	12653
G	G	G	G	G	G	G	12	14824
A	A	A	A	A	A	A	13	14990
C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	15	15093
C	T	T	T	T	C	T	16	15529
G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	A	18	16165

[a]Alleles for haplotypes are presented 5′ to 3′ in each column
[b]PS = polymorphic site;
[c]Position of PS within SEQ ID NO:1,]

2. The method of claim 1, wherein the nucleic acid sample contains the second copy of the individual's TNFRSF1A gene to identify [A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF1A gene, wherein the determining step comprises identifying] the phased sequence of nucleotides present at each of PS1-PS18 on the second copy [both copies] of the individual's TNFRSF1A gene,

comparing the phased sequence of the second copy to the TNFRSF1A haplotypes represented in Table 5; and

assigning to the individual, for the second copy of the individual's TNFRSF1A gene, a TNFRSF1A haplotype selected from the TNFRSF1A haplotypes represented in Table 5 which is consistent with the phased sequence of that second copy.[, and wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

HAPLOTYPE PAIR[a]								PS[b] NUMBER	PS POSITION[c]
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11		
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b] NUMBER	PS POSITION[c]
2/19	3/14	12/15	22/8	2/9	3/21	2/15	12/17		
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	G/G	G/G	T/G	G/G	G/T	G/G	G/G	2	3409
A/A	A/A	A/G	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	G/A	A/G	A/G	A/A	A/A	G/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/T	7	11998
G/G	G/G	G/G	G/A	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/C	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	C/C	C/C	T/C	C/C	C/T	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/G	G/A	A/G	A/A	A/A	A/A	G/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/T	T/T	T/C	T/T	C/T	T/C	C/C	T/C	16	15529
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b] NUMBER	PS POSITION[c]
2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16		
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b] NUMBER	PS POSITION[c]
3/27	22/10	2/16	2/26	22/11	12/7	22/2	22/18		
G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/G	G/G	G/T	T/G	G/G	T/G	T/T	2	3409
A/G	A/A	A/G	A/G	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	A/A	A/A	A/G	G/A	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	T/C	C/C	C/C	T/C	C/C	T/C	T/T	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	A/A	A/A	G/G	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/C	C/T	C/C	T/T	T/T	T/C	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]						PS[b]	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	10	12489
T/C	C/C	C/C	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

[a]Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1.]

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene encoding a TNFRSF1A polypeptide with a domain capable of binding TNFα, wherein the TNFRSF1A isogene comprises nucleotides 2920-4210, 11417-12926, and 14634-16768 of SEQ ID NO:1 except the sequence is substituted by the combination of nucleotides at polymorphic sites 1 to 18 (PS1-PS18) defined by a TNFRSF1A haplotype [is] selected from the group consisting of TNFRSF1A haplotypes [isogenes] 1-27 shown in Table 5, wherein the nucleotide positions of PS1-PS18 in SEQ ID NO:1 and the alleles at each of PS1-PS18 for each TNFRSF1A haplotype in the group are set forth in Table 5; and[the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

ISOGENE NUMBER[a]										PS[b] NUMBER	PS POSITION[c]	SEQ ID NO.	REGION EXAMINED[d]
1	2	3	4	5	6	7	8	9	10				
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
A	A	A	A	A	A	A	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
A	A	A	A	A	A	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	C	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	C	C	C	C	C	C	C	C	11	12653	1	11417-12926
A	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	G	G	G	A	A	13	14990	1	14634-16768
C	C	C	C	T	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	T	C	C	C	C	C	C	15	15093	1	14634-16768
C	C	T	C	C	C	T	T	T	C	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]										PS[b] NUMBER	PS POSITION[c]	SEQ ID NO.	REGION EXAMINED[d]
11	12	13	14	15	16	17	18	19	20				
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	T	T	T	2	3409	1	2920-4210
A	A	A	A	G	G	G	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
G	G	G	G	A	A	A	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	A	G	G	6	4082	1	2920-4210
C	C	C	T	C	C	T	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	T	C	C	C	C	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	G	A	G	A	A	A	A	A	G	13	14990	1	14634-16768
C	C	C	C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	C	C	C	15	15093	1	14634-16768
T	T	T	T	C	T	C	T	T	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	A	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]							PS[b]	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	T	1	3102	1	2920-4210
T	T	T	T	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	C	C	C	G	C	C	4	3603	1	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	T	C	C	C	C	10	12489	1	11417-12926
T	T	T	T	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	15	15093	1	14634-16768
C	T	T	T	T	C	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768

[a]Alleles for isogenes are presented 5' to 3' in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;
[d]Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.]

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the fragment comprises at least 15 [10] nucleotides in one of the regions of SEQ ID NO:1 selected from nucleotides 2920-4210, 11417-12926, or 14634-16768 [shown in the table immediately below] and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, guanine at PS4, adenine at PS12, thymine at PS14, thymine at PS15, adenine at PS17 and adenine at PS18, wherein the nucleotide positions in SEQ ID NO:1 of the [selected] polymorphisms are 3102 for PS1, 3603 for PS4, 14824 for PS12, 15089 for PS14, 15093 for PS15, 15932 for PS17 and 16165 for PS18. [has the position set forth in the table immediately below:

ISOGENE NUMBER[a]										PS[b] NUMBER	PS POSITION[c]	SEQ ID NO.	REGION EXAMINED[d]
1	2	3	4	5	6	7	8	9	10				
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
A	A	A	A	A	A	A	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
A	A	A	A	A	A	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	C	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	C	C	C	C	C	C	C	C	11	12653	1	11417-12926
A	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	G	G	G	A	A	13	14990	1	14634-16768
C	C	C	C	T	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	T	C	C	C	C	C	C	15	15093	1	14634-16768
C	C	T	C	C	C	T	T	T	C	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]										PS[b] NUMBER	PS POSITION[c]	SEQ ID NO.	REGION EXAMINED[d]
11	12	13	14	15	16	17	18	19	20				
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	T	T	T	2	3409	1	2920-4210
A	A	A	A	G	G	G	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
G	G	G	G	A	A	A	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	A	G	G	6	4082	1	2920-4210
C	C	C	T	C	C	T	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	T	C	C	C	C	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	G	A	G	A	A	A	A	A	G	13	14990	1	14634-16768
C	C	C	C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	C	C	C	15	15093	1	14634-16768
T	T	T	T	C	T	C	T	T	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	A	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]							PS[b]	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	T	1	3102	1	2920-4210
T	T	T	T	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	C	C	C	G	C	C	4	3603	1	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	T	C	C	C	C	10	12489	1	11417-12926
T	T	T	T	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	15	15093	1	14634-16768
C	T	T	T	T	C	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768

[a]Alleles for isogenes are presented 5′ to 3′ in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;
[d]Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.]

25. An isolated polynucleotide comprising a TNFRSF1A coding sequence, [wherein the coding sequence is selected from the group consisting of 8, 9, 14, 17, and 19 shown in the table immediately below, and] wherein [each of] the coding sequence comprises SEQ ID NO:2, except for being substituted with an adenine at position 935.[at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Isogene Coding Sequence Number				PS	PS
8	9	14,17	19	Number	Position
C	C	T	C	7	224
A	G	G	G	8	362
T	C	T	T	9	403
G	G	G	A	17	935

[a]Alleles for the isogene coding sequence are presented 5′ to 3′ in each column; the numerical portion of the isogene coding sequence number represents the number of the parent full TNFRSF1A isogene;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:2.]

Please cancel claim 33.

Please add the following new claims:

35. The isolated polynucleotide of claim 20, wherein the isogene encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 and wherein the isogene is selected from the group consisting of isogenes 1,2,3,4,5,6,7,10,11,12,13,15,16,18,20, 21,22, 23,24,25,26 and 27.

36. The isolated polynucleotide of claim 20, wherein the isogene is isogene 19, encoding a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a lysine at amino acid position 312.

37. The isolated polynucleotide of claim 20, wherein the isogene is isogene 8 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a glutamine at amino acid position 121.

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38. The isolated polynucleotide of claim 20, wherein the isogene is isogene 9 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a histidine at amino acid position 135.

39. The isolated polynucleotide of claim 20, wherein the isogene is selected from isogenes 14 and 17 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a leucine at amino acid position 75.

A clean version of the amended claims is attached hereto.